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DEC 04 2000

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SEQUENCE LISTING

<100> Kaufman, Randal J.
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Welihinda, Ajith A.

<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

<130> UMV-1584

<140>

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<150> 60/093,526

<151> 1998-07-21

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 3629

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (97)..(3027)

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<223> Description of Artificial Sequence: Primer

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Met Pro Ala Arg Arg Leu
1 5

ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162
Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
25 30 35

gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
40 45 50

act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
55 60 65 70

cct gcc ttt ctc cca gat cct aat gat ggc agc ctg tat acg ctt gga 354
Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly

75

80

85

agc aag aat aat gaa ggc ctg acg aaa ctt cct ttt acc atc cca gaa 402
 Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
 90 95 100

ttg gtg cag gca tcc cca tgc cga agt tca gat gga atc ctc tac atg 450
 Leu Val Gln Ala Ser Pro Cys Arg Ser Ser Asp Gly Ile Leu Tyr Met
 105 110 115

ggt aaa aag cag gac atc tgg tat gtt att gac ctc ctg acc gga gag 498
 Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile Asp Leu Leu Thr Gly Glu
 120 125 130

aag cag cag act ttg tca tgc gcc ttt gca gat agt ctc tgc cca tca 546
 Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala Asp Ser Leu Cys Pro Ser
 135 140 145 150

acc tct ctt ctg tat ctt ggg cga aca gaa tac acc atc acc atg tac 594
 Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu Tyr Thr Ile Thr Met Tyr
 155 160 165

gac acc aaa acc cga gag ctc cgg tgg aat gcc acc tac ttt gac tat 642
 Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn Ala Thr Tyr Phe Asp Tyr
 170 175 180

gcg gcc tca ctg cct gag gac gaa ggg gac tac aag atg tcc cac ttt 690
 Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp Tyr Lys Met Ser His Phe
 185 190 195

gtg tcc aat ggt gat ggg ctg gtg gtg act gtg gac agt gaa tct ggg 738
 Val Ser Asn Gly Asp Gly Leu Val Val Thr Val Asp Ser Glu Ser Gly
 200 205 210

gac gtc ctg tgg atc caa aac tac gcc tcc cct gtg gtg gcc ttt tat 786
 Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser Pro Val Val Ala Phe Tyr
 215 220 225 230

gtc tgg cag cgg gag ggt ctg agg aag gtg atg cac atc aat gtc gct 834
 Val Trp Gln Arg Glu Gly Leu Arg Lys Val Met His Ile Asn Val Ala
 235 240 245

gtg gag acc ctg cgc tat ctg acc ttc atg tct ggg gag gtg ggg cgc 882
 Val Glu Thr Leu Arg Tyr Leu Thr Phe Met Ser Gly Glu Val Gly Arg
 250 255 260

atc aca aag tgg aag tac ccg ttc ccc aag gag aca gag gcc aag agc 930
 Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys Glu Thr Glu Ala Lys Ser
 265 270 275

aag ctg acg ccc act ctg tat gtt ggg aaa tac tct acc agc ctc tat 978
 Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys Tyr Ser Thr Ser Leu Tyr
 280 285 290

gcc tct ccc tca atg gta cac gag ggg gtt gct gtc gtg ccc cgc ggc 1026
 Ala Ser Pro Ser Met Val His Glu Gly Val Ala Val Val Pro Arg Gly
 295 300 305 310

11/19

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agc aca ctt cct ttg ctg gaa ggg ccc cag act gat ggc gtc acc atc 1074
 Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln Thr Asp Gly Val Thr Ile
 315 320 325
 ggg gac aag ggg gag tgt gtg atc acg ccc agc acg gac gtc aag ttt 1122
 Gly Asp Lys Gly Glu Cys Val Ile Thr Pro Ser Thr Asp Val Lys Phe
 330 335 340
 gat ccc gga ctc aaa agc aag aac aag ctc aac tac ttg agg aat tac 1170
 Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu Asn Tyr Leu Arg Asn Tyr
 345 350 355
 tgg ctt ctg ata gga cac cat gaa acc cca ctg tct gcg tct acc aag 1218
 Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys
 360 365 370
 atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg 1266
 Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val
 375 380 385 390
 att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg 1314
 Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu
 395 400 405
 gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg 1362
 Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val
 410 415 420
 gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gtg gac 1410
 Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp
 425 430 435
 tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg 1458
 Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu
 440 445 450
 att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag 1506
 Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln
 455 460 465 470
 cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc 1554
 Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile
 475 480 485
 cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga 1602
 Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly
 490 495 500
 gac acg gct cag gac ggc gag ctc ctg gac acg tct ggc ccg tac tca 1650
 Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser
 505 510 515
 gag agc tcg ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac 1698
 Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn
 520 525 530

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cac tcg ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc 1746
 His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro
 535 540 545 550

tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt 1794
 Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val
 555 560 565

ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag 1842
 Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu
 570 575 580

ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg 1890
 Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val
 585 590 595

aag agg atc ctc ccc gag tgt ttt agc ttc gca gac cgt gag gtc cag 1938
 Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe Ala Asp Arg Glu Val Gln
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ctg ttg cga gaa tcg gat gag cac ccg aac gtg atc cgc tac ttc tgc 1986
 Leu Leu Arg Glu Ser Asp Glu His Pro Asn Val Ile Arg Tyr Phe Cys
 615 620 625 630

acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca 2034
 Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala
 635 640 645

gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc 2082
 Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly
 650 655 660

ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac 2130
 Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His
 665 670 675

ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc 2178
 Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile
 680 685 690

ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc 2226
 Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser
 695 700 705 710

gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc 2274
 Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser
 715 720 725

cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg 2322
 Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met
 730 735 740

ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt 2370
 Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe
 745 750 755

tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct 2418

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Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro
760 765 770

ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc 2466
Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys
775 780 785 790

agc ctt gac tgc ttg cac cca gag aag cac gaa gac gtc att gca cga 2514
Ser Leu Asp Cys Leu His Pro Glu Lys His Glu Asp Val Ile Ala Arg
795 800 805

gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca 2562
Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser
810 815 820

gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag 2610
Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln
825 830 835

ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
840 845 850

gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
855 860 865 870

aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754
Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
875 880 885

cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
890 895 900

gcc atg aga aat aag aag cac cac tac ccg gag ctg cct gca gag gtg 2850
Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
905 910 915

cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898
Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
920 925 930

tct cgc ttc ccc cac ctc ctc gca cac acc tac ccg gcc atg gag ctg 2946
Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
935 940 945 950

tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994
Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
955 960 965

gag ccc cag ccc cca gtg act cca gac gcc ctc tgagcagagg cgccccct 3047
Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu
970 975

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 ccggaattga gaggtggggg atgtgagga gggggaggac ggagttcaga ggggtgtcgtc 3527
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 35 40 45
 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
 50 55 60
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
 65 70 75 80
 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
 85 90 95
 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
 100 105 110
 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
 130 135 140
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
 165 170 175

Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
 180 185 190
 Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
 195 200 205
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
 210 215 220
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
 225 230 235 240
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
 245 250 255
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
 260 265 270
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
 275 280 285
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
 290 295 300
 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln
 305 310 315 320
 Thr Asp Gly Val Thr Ile Gly Asp Lys Gly Glu Cys Val Ile Thr Pro
 325 330 335
 Ser Thr Asp Val Lys Phe Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu
 340 345 350
 Asn Tyr Leu Arg Asn Tyr Trp Leu Leu Ile Gly His His Glu Thr Pro
 355 360 365
 Leu Ser Ala Ser Thr Lys Met Leu Glu Arg Phe Pro Asn Asn Leu Pro
 370 375 380
 Lys His Arg Glu Asn Val Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe
 385 390 395 400
 Glu Glu Val Ile Asn Leu Val Asp Gln Thr Ser Glu Asn Ala Pro Thr
 405 410 415
 Thr Val Ser Arg Asp Val Glu Glu Lys Pro Ala His Ala Pro Ala Arg
 420 425 430
 Pro Glu Ala Pro Val Asp Ser Met Leu Lys Asp Met Ala Thr Ile Ile
 435 440 445
 Leu Ser Thr Phe Leu Leu Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr
 450 455 460
 Pro Leu Ser Met His Gln Gln Gln Gln Leu Gln His Gln Gln Phe Gln
 465 470 475 480

Lys Glu Leu Glu Lys Ile Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu
 485 490 495
 Pro Phe His Pro Pro Gly Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp
 500 505 510
 Thr Ser Gly Pro Tyr Ser Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr
 515 520 525
 Ser Pro Arg Ala Ser Asn His Ser Leu Cys Ser Gly Ser Ser Ala Ser
 530 535 540
 Lys Ala Gly Ser Ser Pro Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu
 545 550 555 560
 Thr Ser Val Val Ile Val Gly Lys Ile Ser Phe Cys Pro Lys Asp Val
 565 570 575
 Leu Gly His Gly Ala Glu Gly Thr Ile Val Tyr Arg Gly Met Phe Asp
 580 585 590
 Asn Arg Asp Val Ala Val Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe
 595 600 605
 Ala Asp Arg Glu Val Gln Leu Leu Arg Glu Ser Asp Glu His Pro Asn
 610 615 620
 Val Ile Arg Tyr Phe Cys Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile
 625 630 635 640
 Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys
 645 650 655
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr
 660 665 670
 Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
 675 680 685
 Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
 690 695 700
 Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
 705 710 715 720
 Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
 725 730 735
 Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
 740 745 750
 Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
 755 760 765
 Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
 770 775 780

Pub
 8/14

1
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Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
785 790 795 800

Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
805 810 815

Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
820 825 830

Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg
835 840 845

Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
850 855 860

Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
865 870 875 880

Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
885 890 895

Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
900 905 910

Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
915 920 925

Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
930 935 940

Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr
945 950 955 960

Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala
965 970 975

Leu

<210> 3

<211> 977

<212> PRT

<213> Homo sapiens

<400> 3

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Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
35 40 45

Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val

50 55 60
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
 65 70 75 80
 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
 85 90 95
 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
 100 105 110
 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
 130 135 140
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
 165 170 175
 Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
 180 185 190
 Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
 195 200 205
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
 210 215 220
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
 225 230 235 240
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
 245 250 255
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
 260 265 270
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
 275 280 285
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
 290 295 300
 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln
 305 310 315 320
 Thr Asp Gly Val Thr Ile Gly Asp Lys Gly Glu Cys Val Ile Thr Pro
 325 330 335
 Ser Thr Asp Val Lys Phe Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu
 340 345 350
 Asn Tyr Leu Arg Asn Tyr Trp Leu Leu Ile Gly His His Glu Thr Pro

Pub
6/4

a

355 360 365
 Leu Ser Ala Ser Thr Lys Met Leu Glu Arg Phe Pro Asn Asn Leu Pro
 370 375 380
 Lys His Arg Glu Asn Val Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe
 385 390 395 400
 Glu Glu Val Ile Asn Leu Val Asp Gln Thr Ser Glu Asn Ala Pro Thr
 405 410 415
 Thr Val Ser Arg Asp Val Glu Glu Lys Pro Ala His Ala Pro Ala Arg
 420 425 430
 Pro Glu Ala Pro Val Asp Ser Met Leu Lys Asp Met Ala Thr Ile Ile
 435 440 445
 Leu Ser Thr Phe Leu Leu Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr
 450 455 460
 Pro Leu Ser Met His Gln Gln Gln Gln Leu Gln His Gln Gln Phe Gln
 465 470 475 480
 Lys Glu Leu Glu Lys Ile Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu
 485 490 495
 Pro Phe His Pro Pro Gly Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp
 500 505 510
 Thr Ser Gly Pro Tyr Ser Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr
 515 520 525
 Ser Pro Arg Ala Ser Asn His Ser Leu Cys Ser Gly Ser Ser Ala Ser
 530 535 540
 Lys Ala Gly Ser Ser Pro Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu
 545 550 555 560
 Thr Ser Val Val Ile Val Gly Lys Ile Ser Phe Cys Pro Lys Asp Val
 565 570 575
 Leu Gly His Gly Ala Glu Gly Thr Ile Val Tyr Arg Gly Met Phe Asp
 580 585 590
 Asn Arg Asp Val Ala Val Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe
 595 600 605
 Ala Asp Arg Glu Val Gln Leu Leu Arg Glu Ser Asp Glu His Pro Asn
 610 615 620
 Val Ile Arg Tyr Phe Cys Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile
 625 630 635 640
 Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys
 645 650 655
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr

660

665

670

Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
675 680 685

Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
690 695 700

Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
705 710 715 720

Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
725 730 735

Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
740 745 750

Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
755 760 765

Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
770 775 780

Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
785 790 795 800

Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
805 810 815

Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
820 825 830

Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg
835 840 845

Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
850 855 860

Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
865 870 875 880

Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
885 890 895

Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
900 905 910

Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
915 920 925

Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
930 935 940

Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr
945 950 955 960

Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala

Leu

<210> 4

<211> 983

<212> PRT

<213> Caenorhabditis elegans

<400> 4

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Ser Ile Gly Asp Asp Glu Glu Lys Thr Ser Ser Thr Ile Leu Val Ser
35 40 45

Thr Ile Asp Gly Arg Leu Arg Ala Leu Asp Ser Glu Thr Gly Glu Ile
50 55 60

Lys Trp Thr Leu Gln Glu Glu Pro Val Leu Arg Ser Pro Ser Ala Val
65 70 75 80

Lys Gln Gly Phe Thr Phe Leu Pro Asn Pro Leu Asp Gly Ser Leu Tyr
85 90 95

Val Leu Lys Asn Ser Ser Leu Lys Lys Leu Pro Phe Asn Ile Pro Gln
100 105 110

Leu Val His Ala Ser Pro Cys Lys Gly Asn Asp Gly Ile Leu Tyr Ala
115 120 125

Gly Ser Lys Lys Asp Val Trp Phe Gly Ile Asp Pro Lys Thr Gly Leu
130 135 140

Lys Val Glu Tyr Ile Leu Leu Asn Ile Ser Asp Lys Ile Leu Phe Leu
145 150 155 160

Gln Val Glu Thr Leu Ser Ser Ala Ser Ala Asp Arg Ile Cys Pro Ala
165 170 175

Asn Gln Lys Gln Thr Ile Phe Leu Gly Arg Thr Glu Tyr Arg Val Ser
180 185 190

Met Phe Asp Glu Lys Asn Arg Gly Lys Thr Trp Asn Ala Thr Phe Asn
195 200 205

Asp Tyr Ser Ala His Leu Leu Pro Glu Val Asn Thr Trp Pro Phe Lys
210 215 220

His Tyr Ala Ser Ser Ser His Gly Tyr Ile Leu Thr Phe Asp Arg Glu
225 230 235 240

Thr Gly Glu Met Arg Trp Glu Gln Asp Leu Lys Gln Pro Val Val Ala
245 250 255

Leu Tyr Leu Leu Arg Asp Asp Gly Leu His Lys Leu Pro Phe Glu Val
260 265 270

Met Gly Lys Glu Thr Met Glu Asn Val Ala Lys Asn Ile Phe Thr Val
275 280 285

Asp Gln Trp Pro Thr Val Leu Gly Val Asn Ala Ala Asp Pro Gln Thr
290 295 300

Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser
305 310 315 320

Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile
325 330 335

Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala
340 345 350

Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg
355 360 365

Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser
370 375 380

Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr
385 390 395 400

Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys
405 410 415

Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro
420 425 430

Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu
435 440 445

Asn Asn His Pro Ile Pro Phe Tyr Ala Thr Leu Val Thr Met Phe Ala
450 455 460

Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln
465 470 475 480

Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly
485 490 495

Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe
500 505 510

Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val
515 520 525

Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys
530 535 540

Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala
545 550 555 560

Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala
565 570 575

Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe
580 585 590

Cys Met Glu Ser Asp Ser Gln Phe Arg Tyr Leu Ala Leu Glu Leu Cys
595 600 605

Ile Ala Ser Leu Asn Asp Tyr Val Glu Gln Lys Glu Val Gln Gln Asn
610 615 620

Val Thr Ile Ala Leu Arg Asp Ile Met Lys Gln Ala Thr Asp Gly Leu
625 630 635 640

Ala His Leu His Ala Ser Lys Ile Val His Arg Asp Met Lys Pro Gln
645 650 655

Asn Val Leu Ile Thr Met Ala Ser Gln Arg Gly Glu Met Arg Ala Val
660 665 670

Ile Ser Asp Phe Gly Leu Cys Lys Arg Val Gln Pro Gly Lys Asn Ser
675 680 685

Ile Ser Arg Gly Ile Ala Ser Gly Leu Ala Gly Thr Asp Gly Trp Ile
690 695 700

Ala Pro Glu Val Leu Ile Ser Ala Ser Thr Ser Tyr Pro Val Asp Ile
705 710 715 720

Phe Ser Leu Gly Cys Ile Phe Tyr Tyr Val Leu Thr Ser Gly Thr His
725 730 735

Pro Phe Gly Lys Ser Leu His Arg Gln Ala Asn Ile Val Asn Gly Glu
740 745 750

Tyr Thr Leu Asn Lys Leu Ala Asp Leu Asp Asp Trp Ser Leu Ala Asp
755 760 765

Asp Leu Ile Ser Ser Met Leu Asn Val Glu Pro Leu His Arg Leu Thr
770 775 780

Ala Asp Ala Val Leu Asn His Pro Phe Phe Trp Thr Ser Glu Lys Arg
785 790 795 800

Leu Ala Tyr Phe Ser Asp Val Ser Asp Arg Val Glu Lys Glu Glu Asp
805 810 815

Asn Ser Pro Val Val Arg Arg Ile Glu Thr Asp Ala Arg Ile Val Val
820 825 830

Cys Gly Gly Trp Arg Glu Lys Ile Cys Asp Ala Leu Lys Glu Asp Leu
835 840 845

Arg Lys Phe Arg Thr Tyr Lys Ser Phe Ser Val Arg Asp Leu Leu Arg
850 855 860

Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Glu Asp Val
865 870 875 880

Arg Gln Ser Leu Gly Asp Ile Pro Asp Gln Phe Leu His Tyr Phe Thr
885 890 895

Ser Arg Phe Pro Arg Leu Leu Leu His Val Tyr Lys Ala Thr Glu Tyr
900 905 910

Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg
915 920 925

Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys
930 935 940

Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro
945 950 955 960

Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys
965 970 975

Lys Ser Asn Pro Asn Thr Asp
980

<210> 5
<211> 443
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 5
Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val
1 5 10 15

Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met
20 25 30

Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr
35 40 45

Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr
50 55 60

Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu
65 70 75 80

Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu
85 90 95

Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly
100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro
115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln
130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys
145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn
165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser
180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His
195 200 205

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg
210 215 220

Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr
225 230 235 240

Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu
245 250 255

Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu
260 265 270

His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met
275 280 285

Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg
290 295 300

His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys
305 310 315 320

Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu
325 330 335

Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp
340 345 350

Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr
355 360 365

Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg
370 375 380

Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu
385 390 395 400

Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe
405 410 415

Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser
420 425 430

Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser
435 440

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 7
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
cgccatgcc

9

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> N at position 1 may be Thymine or Cytosine

<220>
<223> N at positions 4, 9, 13 and 16 may be Adenine or
Guanine

<220>
<223> N at positions 7, 10, 19 and 22 may be any
nucleotide

<220>
<223> N at position 21 may be Adenine or Thymine

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
nttnctntnn ccnaantcng nnat

24

<210> 9

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
gctctagaac catgccggcc cggcggct 28

a
<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
aggctgccat-cattaggatc t 21

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cattgatgtg catcaccttc ctc 23

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13

cggaattcat cacctatccc ctgagcatg

29

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

cggaattctc agagggcgtc tggagtca

28